```
                .         .         .         .         .         .
  1  GACGCGGCTGGCACTGGGTGGGCGCCCACACGCTCGGCCACAACTCCCGGGGCTTCGGCG   60
  1    R  G  W  H  W  V  G  A  H  T  L  G  H  N  S  R  G  F  G  V   20

                .         .         .         .         .         .
 61  TGGCCATAGTGGGCAACTACACCGCGGCGCTGCCCACCGAGGCCGCTCTGCGCACGGTGC   120
 21    A  I  V  G  N  Y  T  A  A  L  P  T  E  A  A  L  R  T  V  R   40

                .         .         .         .         .         .
121  GCGACACGCTCCCGAGTTGTGCGGTGCGCGCCGGCCTCCTGCGGCCAGACTACGCGCTGC   180
 41    D  T  L  P  S  C  A  V  R  A  G  L  L  R  P  D  Y  A  L  L   60

                .         .         .         .         .         .
181  TGGGCCACCGCCAGCTGGTGCGCACCGACTGCCCCGGCGACGCGCTCTTCGACCTGCTGC   240
 61    G  H  R  Q  L  V  R  T  D  C  P  G  D  A  L  F  D  L  L  R   80

                .         .         .         .         .         .
241  GCACCTGGCCGCACTTCACCGCGGTGAGTCTTCGCAGCCTGCACTACACGGCCCGCCGCC   300
 81    T  W  P  H  F  T  A  V  S  L  R  S  L  H  Y  T  A  R  R  P   100

                .         .         .         .         .         .
301  CCTCCGTCTACACAAGCTCCACGAGGCCCCTGCCCCCTGCCTGTAACAGCTGTGCCCGCA   360
101    S  V  Y  T  S  S  T  R  P  L  P  P  A  C  N  S  C  A  R  T   120

                .         .         .         .         .         .
361  CAGCCTCAGCCAGGCCCCCAACTTCCCGGCGGCACGTCTATTCAGGAAACCTAGGCCCAG   420
121    A  S  A  R  P  P  T  S  R  R  H  V  Y  S  G  N  L  G  P  A   140

                .         .         .         .         .         .
421  CCTTTGCGGGTCACTCTGCGGGCAACATCCCTGATCCTGTGACTTCTGCCTATGCAGCCT   480
141    F  A  G  H  S  A  G  N  I  P  D  P  V  T  S  A  Y  A  A  S   160

                .         .         .         .         .         .
481  CAGCTCAGCCCCAGACCCAGCCAGCCTGTCCTTTCCCCAGCTCCTAATACCTCTACCTTT   540
161    A  Q  P  Q  T  Q  P  A  C  P  F  P  S  S                     174

                .         .         .         .         .         .
541  CCAGCCAAGGCATGGACCCTGACACCTGCCAACAGCCCCTCTGCCCTCACAACCTCAGCC   600

                .         .         .         .         .         .
601  TGGCCTTCATGACTTCTCTACCCAAGTCACAACCTGTCAGGCTGCACCACCTCATCCTGG   660

                .         .         .         .         .         .
661  CCCGCCGAACCTTGACCTCACCCCTGCCCCTACCCGAAGGCTCTCTGTCCACACAACATG   720
```

FIG. 1A

```
                .         .         .         .         .         .
721   AACCTAGGCTGTGACCTTTTGCCTTCACAACCTCTGTCCAGTCCTTAATCCTGTGTTGCA   780
                .         .         .         .         .         .
781   ATTCTCTGTCCAGACAATCTCAACTCTGAGGTTGCTTGTTTCGTCCCTGACTCCTTAACC   840
                .         .         .         .         .         .
841   CCTGATGACAACTCTTATGCCAGCACAACTTTGACCTGATGACCTCATCCCAGCCCTTGA   900
                .         .         .         .         .         .
901   TCGCCATCACTAAAACAATTTTAGAATCACACCTGGACAATCTCGTGCTACCTACATACT   960
                .         .         .         .         .         .
961   GCCACTCCATTTCATTAAGCTATTGACTAGCACATCCATCTCGGCCTATAGTTGGCTTTG  1020
                .         .         .         .         .         .
1021  TCCTCACTCTCTCACTTTGGGCCACTGTCCCCTCCCTGATAAAGGGGATATCACCACCGA  1080
                .         .         .         .         .         .
1081  TCCCACAGAAATACAAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACT  1140
                .         .         .         .         .         .
1041  AGAAAATCTAGAAGAAATGGATAAATTCCTCAACACCCACTACCAAAAAAAAAAAAAAAA  1200
```

FIG. 1B

```
                .         .         .         .         .         .
  1 GCCGTTATGTGAGGTAAGCAGCTTTCTCCAACAGAAGTTCCTCTCTCCTCAAAGGCCCAG   60

                .         .         .         .         .         .
 61 AGTGTCCAGGCCAACCAACTGACCAAGAATTACAACTGCTGAAACTGGCCTCCGAGGTTC  120

                .         .         .         .         .         .
121 TCTGCTGGGTCTGTGCCCTGGAACTGGAGACCCACCATGAAGGCCTGGGGTGCCCTCTGG  180
  1                                       M  K  A  W  G  A  L  W    8

                .         .         .         .         .         .
181 ATCGTGCTTGGATTGCTGCTGTGGCCAGAGCCAGGGGCAGCCTCCTCCTTGCCTCTGCTC  240
  9 I  V  L  G  L  L  L  W  P  E  P  G  A  A  S  S  L  P  L  L   28

                .         .         .         .         .         .
241 ATGGACTCCATCATCCAGGCCCTTGCTGAACTTGAGCAAAAGGTACCAGTGACTGAGGCC  300
 29 M  D  S  I  I  Q  A  L  A  E  L  E  Q  K  V  P  V  T  E  A   48

                .         .         .         .         .         .
301 AGCATCACTGCCTCTGCATGGATTCTGTCAGCCAAGAACTCCAGCACCCACAATTCCCTT  360
 49 S  I  T  A  S  A  W  I  L  S  A  K  N  S  S  T  H  N  S  L   68

                .         .         .         .         .         .
361 CACCAGCGCTTGCTGCTGAAGGCACCAAGCCACAACACTACAGAGCCAGATCCTCACTCT  420
 69 H  Q  R  L  L  L  K  A  P  S  H  N  T  T  E  P  D  P  H  S   88

                .         .         .         .         .         .
421 CTCAGCCCGGAGCTTCAAGCACTGATTTCTGAGGTGGCTCAACACGATGTACAGAATGGG  480
 89 L  S  P  E  L  Q  A  L  I  S  E  V  A  Q  H  D  V  Q  N  G   108

                .         .         .         .         .         .
481 CGGGAATATGGAGTGGTGCTGGCACCTGATGGCTCCACCGTAGCTGTGAAGCCTCTGCTG  540
109 R  E  Y  G  V  V  L  A  P  D  G  S  T  V  A  V  K  P  L  L   128

                .         .         .         .         .         .
541 TTTGGGCTAGAGGCCGGTCTACAGGCACACAGCGTTGCTAACTTGCCTTCAGATTGTCTG  600
129 F  G  L  E  A  G  L  Q  A  H  S  V  A  N  L  P  S  D  C  L   148

                .         .         .         .         .         .
601 GCTATCCCCTGTGATACTGGAGACACCTTGGCCAATATTAGAGCCACCTGGCCAGGACTC  660
149 A  I  P  C  D  T  G  D  T  L  A  N  I  R  A  T  W  P  G  L   168

                .         .         .         .         .         .
661 ATGGATGCTTTTCCAAATGCCTCTTCTCCAGATGTTGGAGCCACTTTACCAAACGACAAA  720
169 M  D  A  F  P  N  A  S  S  P  D  V  G  A  T  L  P  N  D  K   188
```

FIG. 2A

```
                .         .         .         .         .         .
721  GCCAAGACTCCCACCACTGTGGACAGACTCCTGGCAATCACCTTGGCTGGTGACTTAGGT  780
189  A  K  T  P  T  T  V  D  R  L  L  A  I  T  L  A  G  D  L  G   208

                .         .         .         .         .         .
781  CTGACCTTCCTCCACAGGTCCCAGACTTGGAGTCCTCCAGGACTGGGAACTGAGGGCTGC  840
209  L  T  F  L  H  R  S  Q  T  W  S  P  P  G  L  G  T  E  G  C   228

                .         .         .         .         .         .
841  TGGGACCAGCTTACTGCCCCCAGGGTCTTCACACTGTTGGACCCCCAGGCATCCAGGCTC  900
229  W  D  Q  L  T  A  P  R  V  F  T  L  L  D  P  Q  A  S  R  L   248

                .         .         .         .         .         .
901  ACCATGGCTTTCCTCAATGGTGCCTTAGATGGAGCTCTCCTTGGGAACCACTTGAGCCAA  960
249  T  M  A  F  L  N  G  A  L  D  G  A  L  L  G  N  H  L  S  Q   268

                .         .         .         .         .         .
961  ATCCCTAGGCCCCACCCACCCCTCAGCCACCTGCTAAGAGAGTACTATGGAGCTGGGGTG  1020
269  I  P  R  P  H  P  P  L  S  H  L  L  R  E  Y  Y  G  A  G  V   288

                .         .         .         .         .         .
1021 AATGGAGATCCGGTGTTCCGAAGTAACTTCCGAAGGCAGAACGGTGCTGCTTTGACTTCA  1080
289  N  G  D  P  V  F  R  S  N  F  R  R  Q  N  G  A  A  L  T  S   308

                .         .         .         .         .         .
1081 GCCCCTACCCTGGCCCAGCAGGTATGGGAGGCCCTTGTCCTGTTACAGAAACTGGAGCCA  1140
309  A  P  T  L  A  Q  Q  V  W  E  A  L  V  L  L  Q  K  L  E  P   328

                .         .         .         .         .         .
1141 GAACACCTACAGTTGCAGAACATTAGCCAAGAGCAGCTGGCTCAGGTAGCCACCTTGGCT  1200
329  E  H  L  Q  L  Q  N  I  S  Q  E  Q  L  A  Q  V  A  T  L  A   348

                .         .         .         .         .         .
1201 ACCAAGGAGTTCACTGAGGCTTTCCTGGGATGCCCAGCCATTCACCCCCGCTGCCGTTGG  1260
349  T  K  E  F  T  E  A  F  L  G  C  P  A  I  H  P  R  C  R  W   368

                .         .         .         .         .         .
1261 GGAGCGGCTCCCTACCGAGGCCACCCAACACCACTCCGGCTGCCACTTGGATTCTTATAT  1320
369  G  A  A  P  Y  R  G  H  P  T  P  L  R  L  P  L  G  F  L  Y   388

                .         .         .         .         .         .
1321 GTGCATCACACATACGTGCCAGCGCCACCCTGCACCACCTTCCAGAGCTGCGCCGCCGAT  1380
389  V  H  H  T  Y  V  P  A  P  P  C  T  T  F  Q  S  C  A  A  D   408
```


FIG. 2B

```
                .         .         .         .         .         .
1381  ATGCGCTCCATGCAGCGTTTCCACCAGGATGTGCGCAAGTGGGATGACATCGGCTACAGT  1440
 409  M  R  S  M  Q  R  F  H  Q  D  V  R  K  W  D  D  I  G  Y  S    428
                .         .         .         .         .         .
1441  TTCGTGGTAGGCTCCGACGGCTATCTGTACCAGGGCCGTGGCTGGCACTGGGTAGGTGCG  1500
 429  F  V  V  G  S  D  G  Y  L  Y  Q  G  R  G  W  H  W  V  G  A    448
                .         .         .         .         .         .
1501  CACACACGCGGCTACAACTCCCGCGGCTTCGGTGTGGCCTTCGTGGGCAACTACACTGGG  1560
 449  H  T  R  G  Y  N  S  R  G  F  G  V  A  F  V  G  N  Y  T  G    468
                .         .         .         .         .         .
1561  TCACTGCCCAACGAAGCTGCGCTGAACACGGTGCGCGACGCGCTCCCGAGCTGCGCAATT  1620
 469  S  L  P  N  E  A  A  L  N  T  V  R  D  A  L  P  S  C  A  I    488
                .         .         .         .         .         .
1621  CGCGAAGGTCTCTTGCGGCCAGACTACAAGCTGCTTGGCCACCGCCAGCTAGTGCTCACC  1680
 489  R  E  G  L  L  R  P  D  Y  K  L  L  G  H  R  Q  L  V  L  T    508
                .         .         .         .         .         .
1681  CACTGCCCCGGGAACGCGCTCTTCAACTTGCTGCGCACCTGGCCTCACTTCACAGAGGTT  1740
 509  H  C  P  G  N  A  L  F  N  L  L  R  T  W  P  H  F  T  E  V    528
                .         .         .         .         .         .
1741  GAAAACTAAGAACTCCTTTGAGAGACCCTTGAAGATCCAGGAGGTATTATCCCTGATGAT  1800
 529  E  N  *                                                       531
                .         .         .         .         .         .
1801  CCTTTGAGCAACCACAGACCTCCAATAAAGGGACCACTGAAAGGAAAAAAAAAAAAAAAA  1860
                .
1861  AAAAAAAAAAAAAAAA  1876
```

FIG. 2C

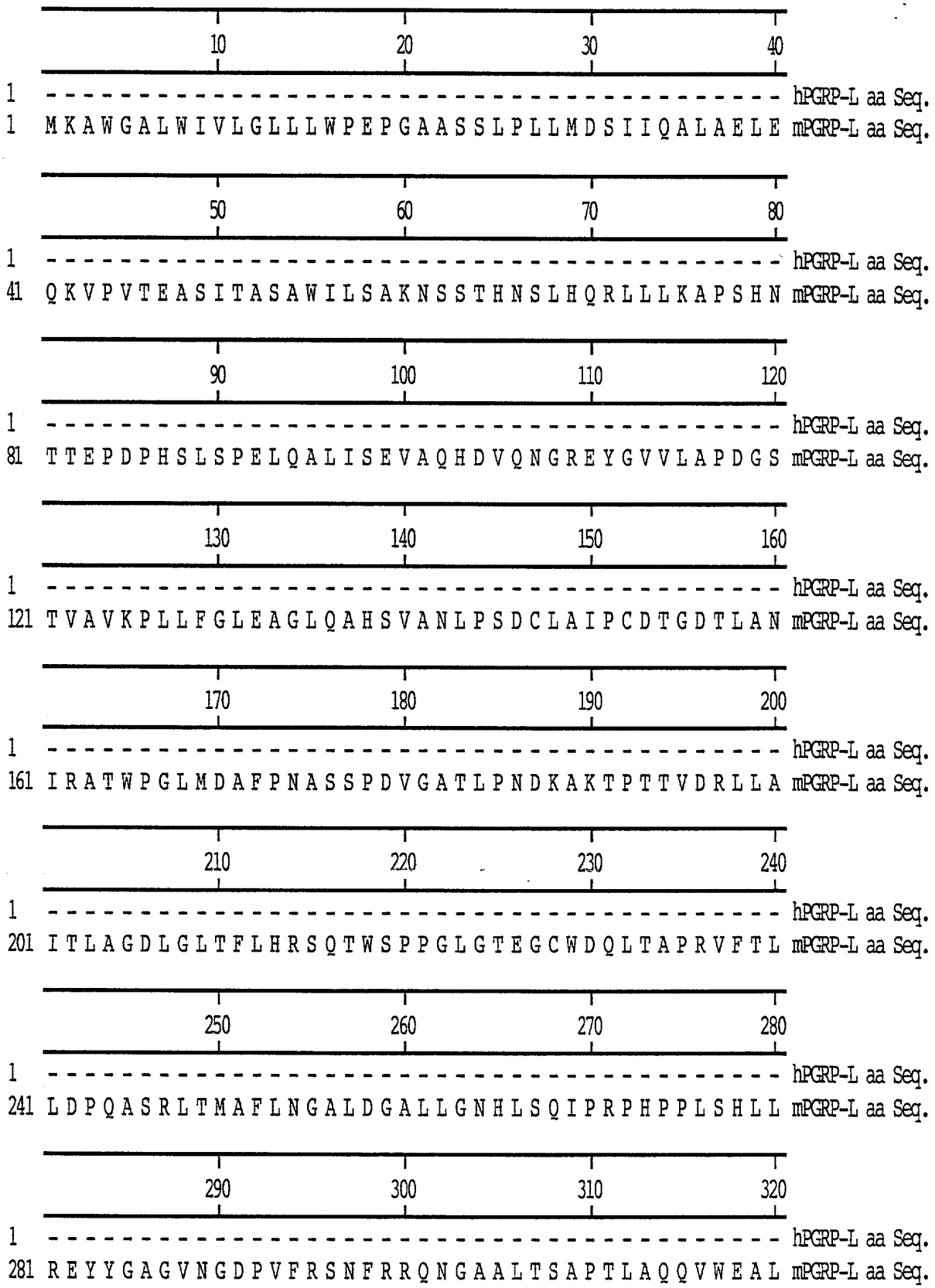

10 20 30 40
1 ---------- hPGRP-L aa Seq.
1 MKAWGALWIVLGLLLWPEPGAASSLPLLMDSIIQALAELE mPGRP-L aa Seq.
50 60 70 80
1 ---------- hPGRP-L aa Seq.
41 QKVPVTEASITASAWILSAKNSSTHNSLHQRLLLKAPSHN mPGRP-L aa Seq.
90 100 110 120
1 ---------- hPGRP-L aa Seq.
81 TTEPDPHSLSPELQALISEVAQHDVQNGREYGVVLAPDGS mPGRP-L aa Seq.
130 140 150 160
1 ---------- hPGRP-L aa Seq.
121 TVAVKPLLFGLEAGLQAHSVANLPSDCLAIPCDTGDTLAN mPGRP-L aa Seq.
170 180 190 200
1 ---------- hPGRP-L aa Seq.
161 IRATWPGLMDAFPNASSPDVGATLPNDKAKTPTTVDRLLA mPGRP-L aa Seq.
210 220 230 240
1 ---------- hPGRP-L aa Seq.
201 ITLAGDLGLTFLHRSQTWSPPGLGTEGCWDQLTAPRVFTL mPGRP-L aa Seq.
250 260 270 280
1 ---------- hPGRP-L aa Seq.
241 LDPQASRLTMAFLNGALDGALLGNHLSQIPRPHPPLSHLL mPGRP-L aa Seq.
290 300 310 320
1 ---------- hPGRP-L aa Seq.
281 REYYGAGVNGDPVFRSNFRRQNGAALTSAPTLAQQVWEAL mPGRP-L aa Seq.

FIG. 3A

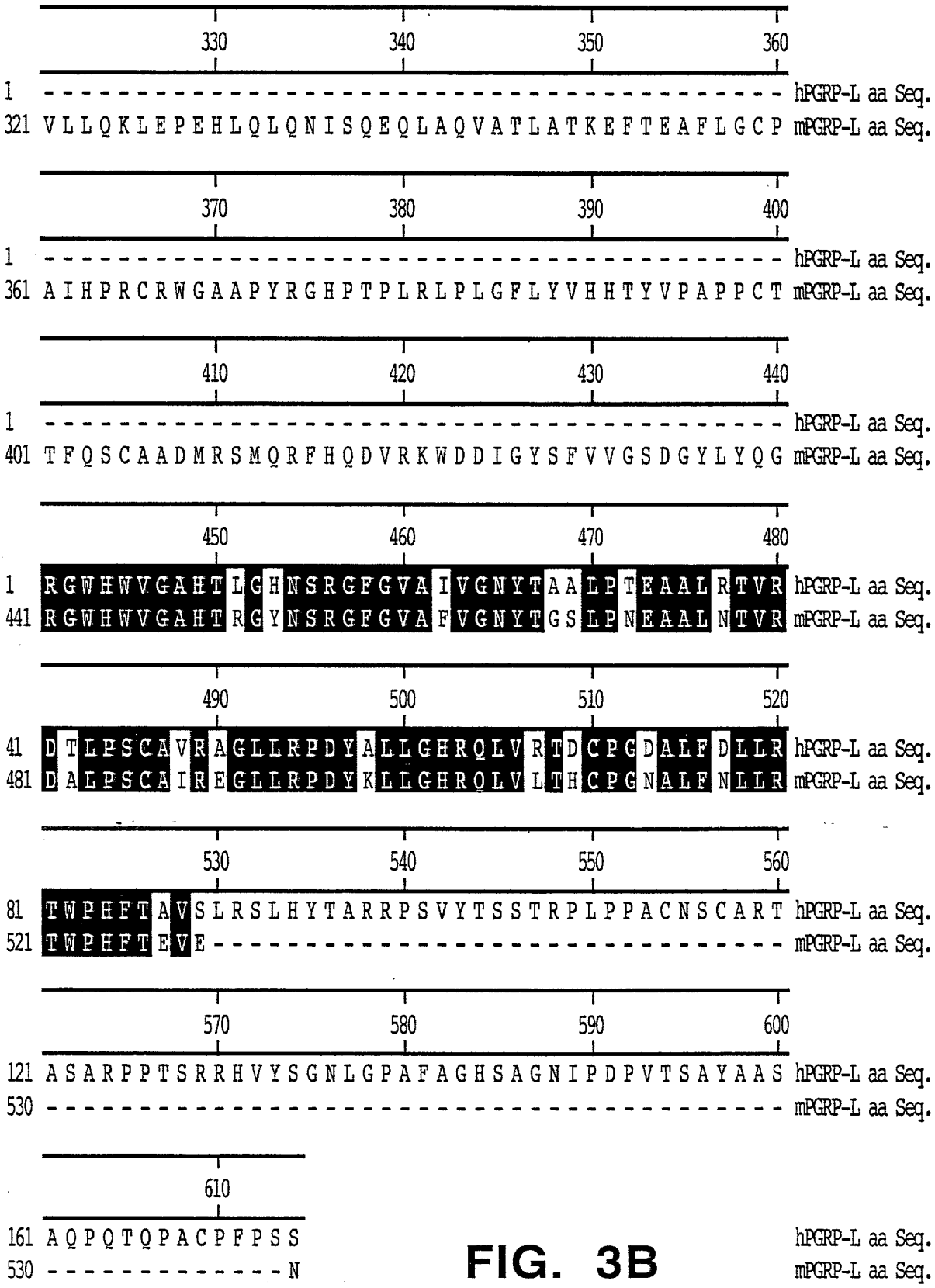
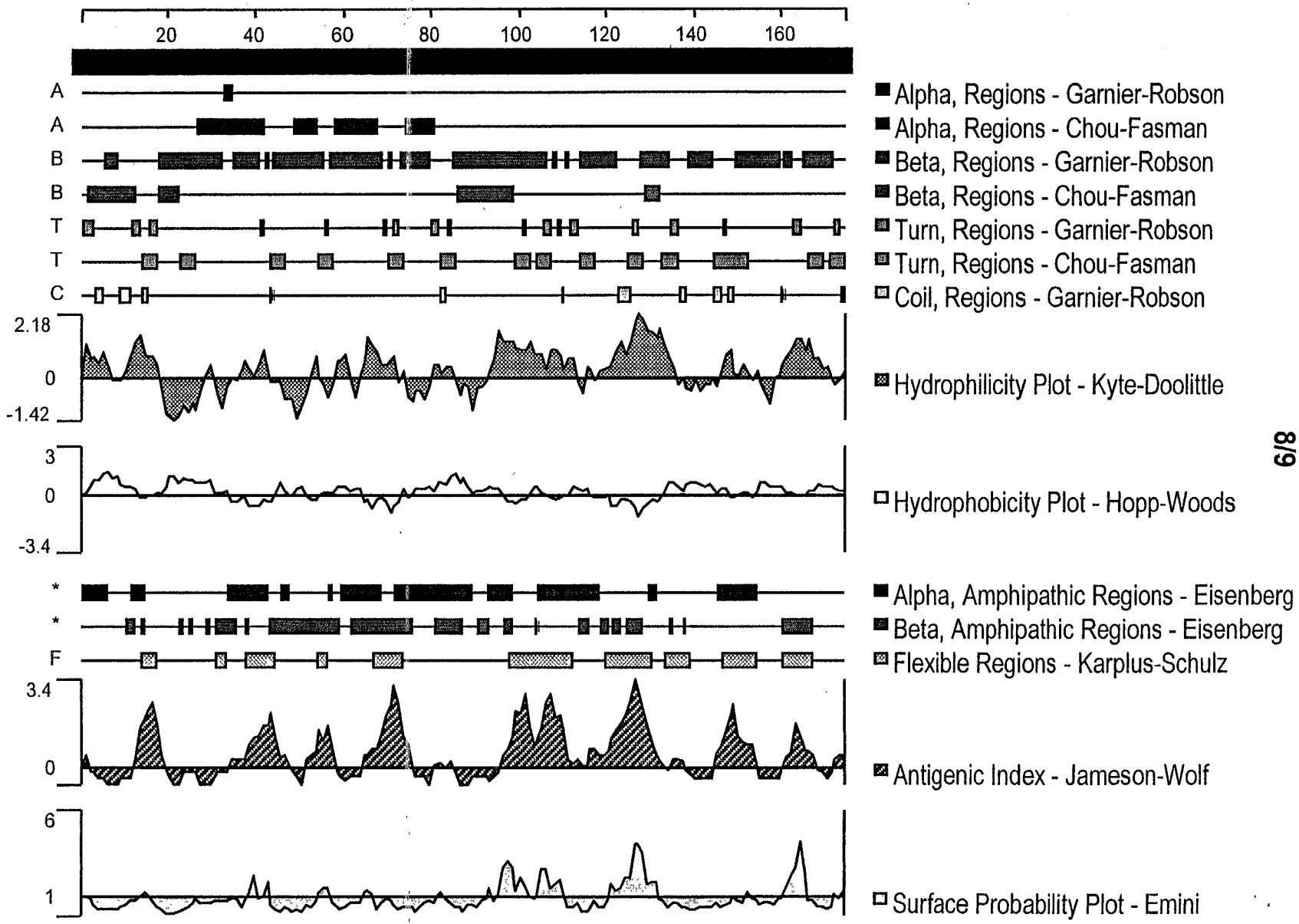

330 340 350 360
1 ---------- hPGRP-L aa Seq.
321 VLLQKLEPEHLQLQNISQEQLAQVATLATKEFTEAFLGCP mPGRP-L aa Seq.
370 380 390 400
1 ---------- hPGRP-L aa Seq.
361 AIHPRCRWGAAPYRGHPTPLRLPLGFLYVHHTYVPAPPCT mPGRP-L aa Seq.
410 420 430 440
1 ---------- hPGRP-L aa Seq.
401 TFQSCAADMRSMQRFHQDVRKWDDIGYSFVVGSDGYLYQG mPGRP-L aa Seq.
450 460 470 480
1 RGWHWVGAHTLGHNSRGFGVAIVGNYTAALPTEAALRTVR hPGRP-L aa Seq.
441 RGWHWVGAHTRGYNSRGFGVAFVGNYTGSLPNEAALNTVR mPGRP-L aa Seq.
490 500 510 520
41 DTLPSCAVRAGLLRPDYALLGHRQLVRTDCPGDALFDLLR hPGRP-L aa Seq.
481 DALPSCAIREGLLRPDYKLLGHRQLVLTHCPGNALFNLLR mPGRP-L aa Seq.
530 540 550 560
81 TWPHFTAVSLRSLHYTARRPSVYTSSTRPLPPACNSCART hPGRP-L aa Seq.
521 TWPHFTEVE---------- mPGRP-L aa Seq.
570 580 590 600
121 ASARPPTSRRHVYSGNLGPAFAGHSAGNIPDPVTSAYAAS hPGRP-L aa Seq.
530 ---------- mPGRP-L aa Seq.
610
161 AQPQTQPACPFPSS hPGRP-L aa Seq.
530 ----------N mPGRP-L aa Seq.

FIG. 3B

FIG. 4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40
60
80
100
120
140
160
A
A
B
B
T
T
C
2.18
0
-1.42
3
0
-3.4
*
*
F
3.4
0
6
1
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini

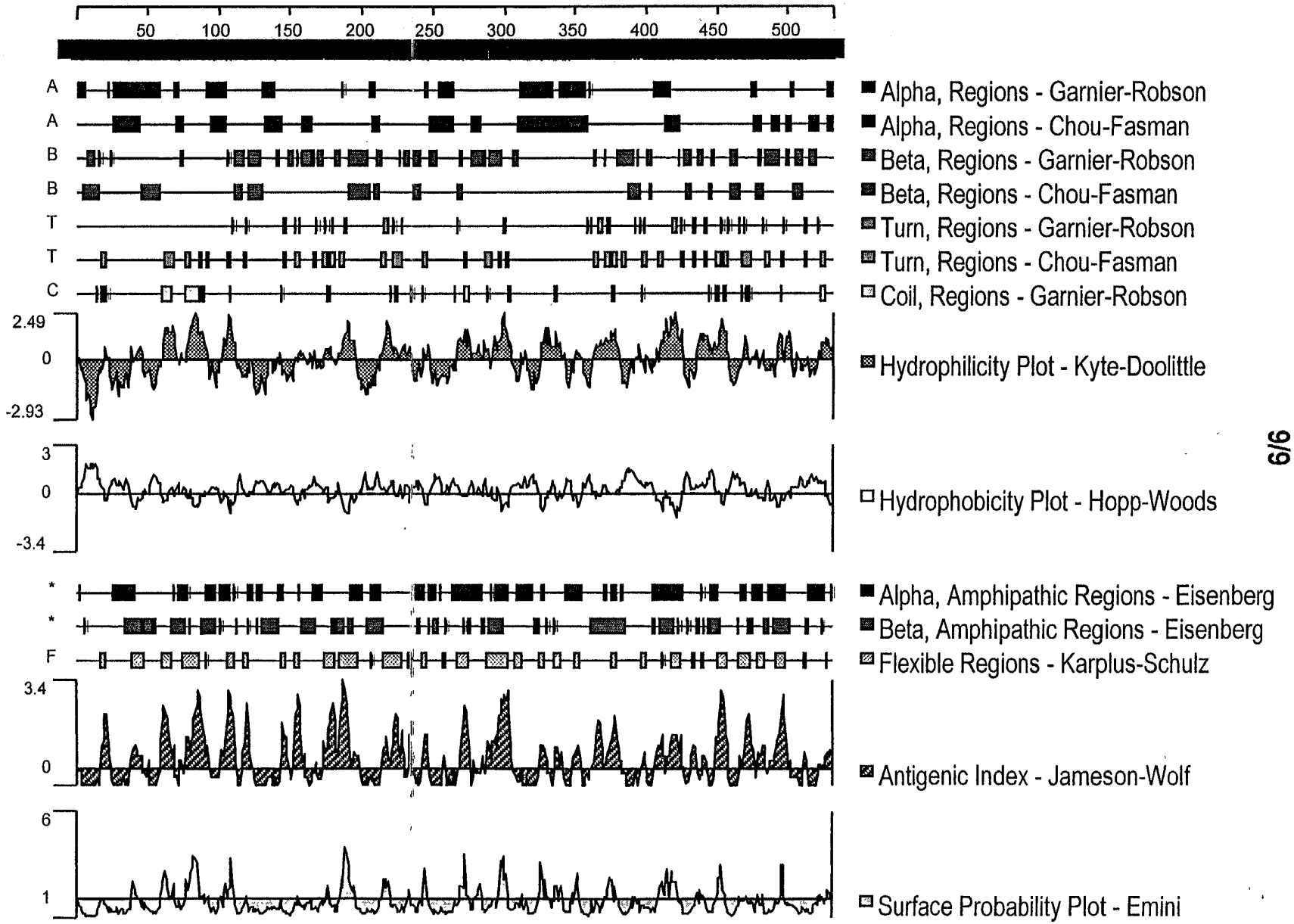

FIG. 5